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Integrative analysis of DNA phylogeography and morphology of the European rose chafer (*Cetonia aurata*) to infer species taxonomy and patterns of postglacial colonisation in Europe

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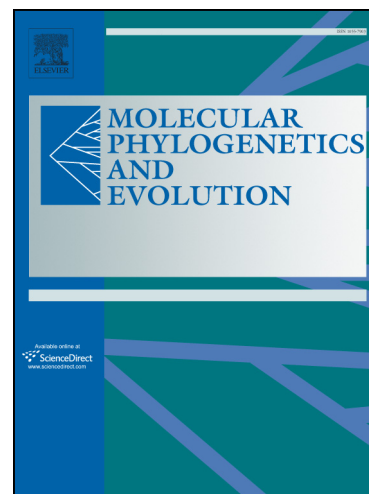
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2 **European rose chafer (*Cetonia aurata*) to infer species taxonomy and**  
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18 **Abstract.** Integrative taxonomy has been proposed as a framework to unify new conceptual  
19 and methodological developments in quantitative assessment of trait variation used in species  
20 delimitation, but empirical studies in this young branch of systematics are rare. Here we use  
21 standard phylogenetic and parsimony network analyses on nuclear and mitochondrial DNA  
22 (*Cox1*, ITS1) of 230 individuals from 65 European sampling sites in order to deduce  
23 population structure of *Cetonia* beetles from geno- and haplotypes. Statistical measures of  
24 population differentiation are inferred on genealogical and geographical scales to test  
25 hypotheses about species limits and population history. By combining results of phylogenetic  
26 structure with features of morphology, including genital shape morphometrics and discrete  
27 external body characters, as well as with measures of population genetics, we attempt to  
28 integrate the results as a test of the validity of species limits, in particular of currently  
29 recognized subspecies. Despite high *Cox1* divergence between some haplotype lineages, even  
30 some sympatric lineages (9%, e.g. N2 vs. N4), nDNA and morphology, as well as pattern of  
31 geographical and genealogical divergence measured by AMOVA analysis did not support the  
32 hypothesis of separate species. Highest divergence in nuclear markers was found among  
33 Italian populations of *C. aurata pisana* and *C.a. sicula*, and moderately high fixation indices  
34 along measurable morphological divergence suggest the correctness of their status as

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